

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA
TTAAACAAGGCTGGCCTTGTACTTGGAATACTGAGTTGTTTAGGACTTTCATTGTGGCAAACCT
CCAGAAAACAACCCCTTTTGTGTCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTTCCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGAATGAAAGGATAAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTAAAGGATATCAT
CAAGAAGACTATTA AAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFFGFFLT YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCCTTATTTTCACTGGAAAATGAACCTGTGTGAATTCTGCTGATCCTGG
TTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGTTTCTGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAAAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAAATTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTTGGTCCCAACATTTCTTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATATAACTACTGAAGTCCTTGGAGAAGTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTA
GATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC
ATTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTTAAGGTTACATGGAAAAGGTTATAGCTTG
CCTTGAGATTGACTCATTTAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTGCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGV
LNSSSRYPFWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLEFSCLLWLTFMYFFWKLGBP
FPILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDAL EELS RQ
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTCKFFYAISSSKSSNVIVLLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
GTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
GTCATGCAGAATTATGGGGATCACCCCTTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
AAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGCCCGCAAGGACCAAGTTGAAACAGCC
TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAG
GATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGA
GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
ATTATCACCACCAAAGATCCCATATTCAACACTCAAACGCAACACAAACAAGAATTTATTGT
CAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTC
CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTTGTGTACAGAAGTTTTATG
GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAATAAAGCAGCATTCAAGAATGA
AGCTGCTGGGTTTGGAGGTGTCCACGGCTCTGCTAGTGCTTGCTCTCCTCTCTTTGGTGCTG
CAGTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT
CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAA
TGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC
GATGCTTGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT
CATGCTCCTTACCCTGCCCGAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAGAAAAGTCCA
CCCTTGGTTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT
GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCT
TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGAC
CTAAACATCTCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTG
AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCCTTCTTCA
GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGTAAGAGCAAAAGAAT
GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAA
GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC
ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
AAAATAAAACCTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC
AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAACTAAT
TTTTATTTTGTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT
TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC
ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAGGACTGAGAGATGCAGAAATATT
TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

FIGURE 6

MARCFSLVLLLSIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYN
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFFFTNKNQKEMIETKVVKEEKANDSNPNNEESKKTDKNPEESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCCGCCCCACCGCGCGCTCCCGCATCTGCACCCGCGAGCCCGGC
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCGGGGCGG
CGCTGCGGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGTCCAGTCAAGCCCGGCCG
GCTCTCAGCTACCCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACATGAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGCTGTGGAGACCA
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCTGTGTGC
ACACCCCTGCCGCTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCC
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGGCTG
CCGCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA
CATCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTAGCT
CCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTCTTGGGAGAGTCAGGCAGGTTAAACTGCA
GGAGCAGTTTGGCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTTGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC
TGATTGGTTTTTGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAAACATCAACCTGGCAAAATG
CAACAAATGAATTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCTCTCTCAGCACAGCCTGGGG
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGTCT
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCATCTGGAATTAAGGTCAAACCTAATCTCACATCCCTCTAAAGATAAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGCGAGCCGTCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTATGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEAAAASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMCLTRDSECCGDQLCVWGHC
TKMATRGSNGTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEdle
RSLTEEMALGEPAAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCACCTTGTGAACCTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTCTGGACCCTT
AACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAGATAGCCGGGTCACTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
ATTGTCAGGGTGGTCGTCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGGTCTCTGCTTCTTTTTTTCTCCGGTCGCATCCCGGGGTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCTAT
GTCATCGCCAGCGCTTCTTCAGCGTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTT
GGAAGACCTGGAGCGGAACAACGGCTCCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCACCCCAACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAACAAAACAAACAAACAA
AAGATTTTATTAAAGATATTTTGTTAACTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLFWTL
NWVLALGQCVLGAFASFYWAFHKPQDIPTFFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
IVRVVVLDKVTDLLLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC
TCCCTGCTCAGCTGCGCGTCCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC
CAGCCGCAACTCCACCGTGAGCCGCTCATCTTACGTTCTTCTCTTCTGCGGGTGCTGGTGTCCA
TCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC
GGGATCCCCACCGTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
CATGTGCTTCGCCACGGCGGCTTCTTCTTCTTCTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA
GCCGGGACCCCGGGTGCCATCCAGAATGGGTTTTGGTTCTTTAAGTTCTGATCCTGGTGGGCCTC
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTACCACATCTGGTTCTACTTCGGCGTCGTGGG
CTCCTTCTCTTATCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGT
GGCTGGGCAAGGCCGAGGAGTGGATTCCCGTGCCTGGTACGAGGCCTCTTCTTCTTCACTCTCCTC
TTCTACTTGCTGTGATCGCGGCGTGGCGCTGATGTTTACTACTAGAGCCAGCGGTGCCA
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGCCATCGCTGCTGCTGCG
CCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCTCTACACCATG
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCATTTGCCAACCCAGCT
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
TGGGCCTCATCATCTTCTCCTGTGCACCTCTTTCATCAGTCTGCGCTCCTCAGACCACGGCAGGTG
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGT
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
ACTTCTGCCTGGTGTGCGCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG
ACCCGGAAGATGATCAGCACGTGGACCGCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
CCTCTACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCTCA
CAGCCTGCCATCTGGTGCTCCTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
CCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCTGAGCCGGGC
CTTCTAGTCGTAGTGCTTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
ACCCACACGGTGGAGCTGCCTCTTCTTCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGTGCTGGAGAGAGCGGGGAAGTCCCACCACAG
TGGGGCATCCGGCACTGAAGCCCTGGTGTCTGCTCACGTCCCCCAGGGGACCCTGCCCCCTTCTCTG
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAACAAGCCAGTGCGTGTAAAAAAA

FIGURE 12

MGACLGACSLSCASCLCGSAPCILSCCPCASRNSTVSRLIFTFFFLGVLVSIIMLSPGVESQL
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQRWLGAKE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAAACEGRAFDNEQDGVITYSY
SFFHFCLVLASLHVMMLTNWYKPGETRKMISTWTAVWVKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGCCGCCAGGAACCCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCCTCCTCCAGGATGAACCCACCTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTCACCTTTGACCTCTTATTTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCCATATGCTGTGTGCAG
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTTCATC
CTTGCCCTGGATTGAGACGTGGTTCTTGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTTCCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAAGTATGAGTACTACTTTTGTAAATGTGAAAAACCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTCAC
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTTCTGTTTTGCATTATGTGTATGCCCTGAAGTGTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTCCAGCCAATTTCAATTAAAATGAA
CTAAATTAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG
 CCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCGCCGCTCCCGGGACAGAAGATGTGCTCCAG
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGGGCTGCCCAT
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCCCAGGGGACCACGGTGCCC
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
 AGGCAGCTTTTGGCGGCTGCCGGGCTGCAGCTCCTGGACCTGTACAGAACCAGATCGCCAGCC
 TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCTCGAGCGCCTCTACCTGGGCAAGAA
 CCGCATCCGCCACATCCAGCCTGGTGCTTCGACACGCTCGACCGCTCCTGGAGCTCAAGCTGC
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGC
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC
 TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACG
 CGCCTGCGGCTGGCCGCAACACCCGATTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGC
 TGCCCTGCAAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCTGCTGGCGACCTCTCGGGCC
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC
 TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCA
 CTTCGCCCAAGAACGCTGGCCGCTGCTCCTGGAGCTTGACTACGCGACTTTGGCTGCCAG
 CCACCACCACCAAGCCACAGTGGCCACCACGAGGCGCTGGTGCGGGAGCCACAGCCTTGTCT
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCCGCCCTC
 CACTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGTGTGTGCCCCGAAGGCTTCACG
 GGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACAGGCCAGCCCTACACAGTCACGCCGAG
 GCCACCACGGTCCCTGACCTGGGCATCGAGCCGCTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA
 GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTTGGGGCCCGGGCGGGTGCCGAGG
 GCGAGGAGGCTGCGGGGAGGCCATACACCCAGCCGTCCACTCCAACCACGCCAGTCACC
 CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCCGGGTGTCTCTGGCCGC
 GCTGGCTGCGGTGGGGGCGAGCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG
 ACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCCTTGGAG
 CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
 ACTCATGGGCTTCCAGGGCTGGCCTCCAGTCACCCCTCCACGCAAAGCCCTACATCTAAGCCA
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAAGTGGCCAGCCCCCTCTGCTGCC
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
 CTAACGTCCCCAGAACCAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
 CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC
 TCCAGGCGGACCCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCT
 GGGAAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAA
 GGCTTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVP LLLPL LLL L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
A L R L A G L G L Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q G T R P S P T P
V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y
T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P G P K A T E G G G E A L P S G S E
C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGG
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTCACAG
AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
TTTCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAAGTGAATGAAAATCCTTAATGGAAG
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG
GCAGCGAGAGAGATGTTTGAAGAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTGG
CTTTCTGTATGCCTCTGGACTTGGTGTTAATCAAGTCAGGCAAAGGCTCTTGTATATTATACAT
TTGGAGCTCTTGGGGCAATCTAATAGCCCATGTTTTGGTAAGTAGACTTTAGTGGAAGGCT
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTTTTCAGCTTTCATGATC
CAGATTTGCTTGTTAAGACCAAATATTCAGTTGAACCTCCTTCAAATTCCTTAAATGGATAT
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTTCTTTAAATGATTAG
TTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA
AAATTTGTAAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTTGAACAATGC
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAAATGACTCCAGAGAGCTCTACTTTCTG
TTTTTTACTTTTCATGATTGGCTGCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTCTTTGCTAATTTGG
AAGATTAACTCATTTTAAATAAAATATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 18

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESESEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAEEMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERVSYALLFGDYL PQNIQAAREMF EKLTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTFGALGGNLI AHMVLVSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAGCCCATTCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAGACATCACTG
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT
AAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGT
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGGAAAGTTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKVQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMK
AFGVHVSCIEPGLFKTNLADPVKVEKKLAIWEQLSPDIKQQYGEgyIEKSLDKLKGKNSYVNMD
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAE LANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAAGTAAAA
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
CATTTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT
CGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGCAGGAGCATT
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
ATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT
GCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGATCCTTAAAGGAGG
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAACAGATTAAAACGAGAAATTGA
GAAAAGGAGAGGAGCACAGATTGAGGCAGCAAGAGAGAAGAACATCCAAAAAGACCCCTCAGGAGA
ACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTCATGTGTT
ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACACCACCATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
CTACATTTTGATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC
TGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCTTACACAG
ACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
GAGACCATGTCTATTAAAAAATAAAATGGAAGCAAGAATAGCCTTATTTTCAAATATGGAAA
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
AAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTTIDIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV
QTHSSKFFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLDQTQDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGCGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA
 GCAGCGCGCAGCGAACGCCCGCCCGCCACACCCCTCTGCGGTCCCGCGGCGCCTGCCACCCCTTCCCTCCTTCCCC
 GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTGCTGCCCCGCGAAACCCGAGGTCAACAGCCCGCGCCTCT
 GCTTCCCTGGGCGCGCGCCCTCCACGCCCTCCTTCTCCCTGGCCCGGCGCCTGGCACCAGGGGACCGTTGCCTGA
 CGCGAGGGCCAGCTCTACTTTTCGCCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACTCCAACCTCCTTCTCCC
 TCCAGTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCGCTTCCCGTCCGGTCCCAAA
 GGTGGGAACGCGTCCGCCCGCGCCGACCAATGGCACGGTTGCGCTTGGCCGCGCTTCTGCAACCTGGCAGTGCTC
 AGCGCCGCGTGTGGTGGCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCACGCTCTTACGTGTCCAAAGGCTTC
 AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCT
 CAAGAGATGGAGGAGAATACAGCCTGCAAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG
 CAAGCTGTCTTTGCTTACGTTACAAGAAGTTGATGAATCTTCAAAGAAGTACTTGAAGATGCAGAGAAATCCCTG
 AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG
 AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG
 TTCCGCTGGTGAAGTCCAGTACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
 CCCTTCGGAGATGTCCCTCGCAAATGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTTCGCTCAAGGC
 TTAGCGGTTCGGGAGATGTCTGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCCGTGTACCCATGCCCTGTGAAG
 ATGATCTACTGCTCCCACTGCCGGGGTCTCGTGACTGTGAAGCCATGTTACAAGTACTGCTCAAACATCATGAGAGGC
 TGTGTTGGCCAAACAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
 GAGGGTCTTTCAACATTGAATCGGTGATGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
 AATAGTGTTCAGTGTCTCAGAAGGTTTTCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
 TCCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCAACACAGCAGCTGGCACT
 AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCCTTCGAGCAAC
 GTTGGCAACGATGAGAGGATGGCTGCAGGAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
 CTGTTTGCAGTGACAGGAAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAACACAGAC
 ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
 GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
 TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA
 CAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTTCTGTTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTCTGAG
 AAAAGTGTTCATCAAAAGTTAAAGGCCACAGTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA
 TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTCAAGTTTTGGG
 AGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
 CTATAGTTAGTTGTGATTTGTGATTTTATCACTCTATTATTGTTTGTATGTTTTTTCTCATTTCGTTTGTGGGTT
 TTTTTTCCAACGTGTATCTCGCCTTGTCTTACAAGCAACAGGGTCCCTTCTGGCACGTAACATGTACGTATT
 TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRL
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQCGGPPKPLPAGRISRISISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCCATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTGAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCACCTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT
AGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGCTG
CTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCCTTCATGTGGCAGCAAGTTTTC
GAGCCCACCTGGAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTA
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC
CCAATGTTGTCCCTTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYLMVLTTPKSNRKMESKKRELFSSQIKGL
TGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDDVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFPEPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLVPVGPVHMGKAVKQSFSSKALICSFPSL
QLEQATHQPIYLPRLGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCCGTGCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTATTAAGAAATT
GTTCCCTTCCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAATCATGTCGG
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
TTCAGATTTCATCACCACCCTTCTGGTTTCACATTTTCATTTCATTGGTTATTTTGGGATTGTTGTT
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT
ATGGAAGGCGGCCAAGTGGAATATAAGCCCCTTTCGGGCATTTCGGTACATGTGGTCGTACCATTT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
TGGTTACTTGTATTTCACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTTCGTCTCTC
TCCATTCTCTTCTTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAG
GATTCCGAGAATCATGTGCATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAACGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
ATTCAAAATCTTGTCCAAGAACTCAAGTCACCTTACATCTATTAAGTCTTTGGAGACTTCATAA
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTATCTGTGTTTGAACTGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTGATC
TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
TTAAAAGACCTAATAAACCCCTATTCTTCCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDLSIE
LDTERENMKCVLGFAIVSTGITAVLLVLI FVLRRRIKLTVELFQITNKAISSAPFLLFQPLWTF
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA
GAVVTCYFNRSKNPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVVHSLVVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTTAGA
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAAATATTCATTCTGTGTGGT
 GAAAATTTTTTGAAGAAAAAATTGCCTTCTTCAAACAGGGGTGTCATTCTGATATTTATGAGGAC
 TGTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGGTGGTGAAGTGGAGTAC
 ATTCAAACAAAGAAACGGCAAGAAGATTAAAAGGCCAAGTTCAGTGTGCCTCAGATCAACTGC
 GATGTCAAAGCCGGAAAGATCATCGATCTGAGTTCATTGTGAAATGTCCAGCAGGATGCCAAGA
 CCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCTACTCCAGTGTGTGTGGCGCTGCCG
 TACACAGTGGTGTGCTTGATAATTGAGGAGGAAAAATCTTGTTCGGAAGGTTGCTGGACAGTCT
 GGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC
 CACCTTGCCAAGGCCATCCCTTCTGCTGCTTCTACCACCAGCATCCCCAGACCACAATCAGTGG
 GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCC
 AGAGCTGATCCAGGTATCCAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC
 GGATGTGAGCCTGGGACTTGTTCAAAAGAAAGATTGAGCACACAGTCTTTGGAGCCAGTATCCC
 TGGGAGATCCAACTGCAAAATTGACTTGTGCTTTTAAATTGATGGGAGCACCAGCATTGGCAAA
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGC
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACAC
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT
 GTAGGTGCGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCAAAGCCAATGGAACAGAAGCGG
 GGCTCCCAATGTGGTGGTGGTATGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCTTCAA
 GACTTGCGAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAG
 AAGCAGTATGTGGTGGAGCCCACTTTGCAAAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC
 GCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCTGCAGCCTCTGGTGAAGCGGGTCTGCG
 AACTGACCGCTGGCCTGCAGCAAGACCTGCTTGAACCTGGCTGACATTGGCTTCGTCATCGAC
 GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGTTTGTGACCAACCTCACCAA
 AGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC
 TGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC
 TACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA
 GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCAGCGGAGGTCTTACGACGACGTCC
 GGATCCCAGCCATGGCTGCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCCTGGGCT
 GCGCAAGAGGAGCTAGAAGTCATTGCCACTACCCCGCCAGAGACCACTCCTTCTTTGTGGACGA
 GTTTGACAACCTCCATCAGTATGTCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC
 AGCCTCGGAACCTGAATTTCAGAGCAGGCAGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTT
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC
 AAATGTCTTGTATTATTCTTTGCCATCATGCTTTTTCATATTCCAAAACCTTGGAGTTACAAAGA
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT
 TTTGACAATTGTTTTCAAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG
 AGCTTTTGTGAGATTTTTAAGTTGTTATTCTGATTTGAACTCTGTAACCCCTCAGCAAGTTTCAT
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAAATGTTTAGAAGGATGAAAAATAAAAAA
 AA
 AAAG

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVYGTVDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR
ESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPGSAAFQKP
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPATFNKTHNTSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTLPVLRVCDTDRILACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISDTRIGAVQYTYEQRLFEGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAQEELEVIATHPARHDSFF
VDEFDNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTATAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC
 CAAACCATGTCTTTTTTCTGTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT
 ACAGAAAAACAACAAAACTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC
 GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCGAGTGTA
 AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTA
 GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC
 CTCAGCCTTCCCACTACAATGTGATAGAACCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA
 CAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAATCCATTCTGGTCATTCT
 TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTAAAAAAGTCT
 TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTGGC
 ATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA
 ACCTGACCTTGAAGAACATTATGGCATTGAGGTGGGTAAGTGAAGTTTGGCCCAATGCCAAGTACGTAATG
 AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
 GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATCCTATAGAGGATTTTACCAAAAACCCATATTT
 CTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAATGTCCAGAGAT
 TTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTTGAAGATGTTTATGTGCGGAT
 CTGTTTGAATTTATTAAAGTGAACATTCATATTCAGAGACACAAATCTTTCTTTCTATATAGAATCC
 ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT
 TGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAAGTTTCTACATTCTACAAAAGCCTAGAAGGACAG
 GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTT
 ACACTGAACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTCAGG
 CCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG
 ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCA
 CTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA
 TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACCTCTTCACTGAAGTTATA
 CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT
 ATTATTTAAAAATTACTTCAACTTTGTGTTTTTAAATGTTTTGACGATTCAATACAAGATAAAAGGATAG
 TGAATCATTCCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
 TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTGTAAATATTTTACTGTGGT
 AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQAEKEDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLLKVNHIPEDTNLFYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
TCGTCCTTGCCAAGAGAGTACACAGTCATTATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATGTGTCGGGAGTGCTGTG
AATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAAGTCAAGAGCTGCCGAAATGGCTCATGGGGGGT
ACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG
GCCAGGTTCTGCGAGCCCCAAAGGTCAGATTTTGTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTATGC
TAAACCTGGGTTTGTCACTCAACTAAGATTTGTATGTTGAGTCTGGAGTTGACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGTATGGAGACAACCGGATGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG
GATCCTCACTCCACGTCTCTTCCACTCCGATGGCTCCAAGATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC
ATGCTCCTCATCCCTTGTTCATGACGGCAGTGCCTCTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTTGGGGGCCAGTCAATGGGTACCAGAAAA
TAACAGGGGGCCCTGGGCTTATCAACGGAGCCATGCTAAAATTGGCAGCGTGGTGTCTTTCTTTTGTAACTCCTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAGCCTGCCGA
GAACCAAGATTTAGACCTGGTGAGAGGAGAGTCTTCCGATGCAGGTTCACTCAAGGGAGACACCATTACACAGCTAT
ACTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGGCCCTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGG
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCTGCATCCCTATCTGCGGGAATTTGAGAATCATCTGCTCCAAAGA
CCCAAGGGTTGCGCTGGCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCTTACACAAGGAGC
GTGGTTCTAGTCTGCAGCGTGGCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACGTGTTACTGACCTGGGGAAG
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATCTACCGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATTTGCTATCCCACTATGACCCCATCTGCTTGATGCTGACATCGCCATCTGAAGCT
CCTAGACAAGGCCGCTATCAGCACCAGTCCAGCCATCTGCCCTGCTGCGCAGTGGGATCTCAGCACTTCTTCCAGGAG
TCCCACATCACTGTGGCTGGCTGGAATGCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTCTCCCGGA
CGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTCAACAAGTGTGCTTAAAGACTGGATTGAAGAAATATGAAATGAACCATGCTCATGCACCTCTTGAAG
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAAGTGTGATTGCGCTGTGAACCTGGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCCAAATGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGTCTTCCCAACTTTTCAAGTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCCTTTGAGGCTCTCAAGTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTT
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTAATAAAATAAGGGTTGGCTTCT
GAACTACAAAAA
AAAAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGGII
KRVCGNERPAPIQSIGSSSLHVLHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSYVLSGNE
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPVQVSRETPLHQLYSAAFSKQKLSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPGQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFQESHITVAGWNVLADVRSPGFKNLTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSVSYDKTCSHRLSTAFTKVLFPKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGC
TGGTCTTGCCCTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCTGTATTAGAACTCTGTA
AAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
TCACAGCCACGGCTCCCTCCCGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCTGGCCTAGACA
ACCTTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA
GGGCACGGCCCTTGTAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA
GGACAAGAGCGGGAGTGAGTTGCCAACCATGCCGACCAGGGCAGGAAAATTCTGAAAACACCACTGCCCTGAAG
TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAA
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCA
GCAGGAACATGGACAGGCCCGGATGCCACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGGAAATAAACTGGTGCAGAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCAGAAAGTGCGGCTCATCTGATTGAGGCCAGTGAAAGACGTGTACCTCGTGTGTCGCCAGGTTCCGCGAGC
GGAGCCCTGACATCTTTCAGGAAGCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACA
CTCCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCAAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTTGAGCCCGGAGGAG
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGTCGAACTGACAGAGGTGAGCC
GGAGTGAGGAGTGGCATTATTGAAAAGAACATCCTCGATAGTACTCAAAGCTTGGAAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCCAGTACTGGTCCCCATCCT
GGGTGATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
TGGGCTTCTGCATTGTAGGAGTTATGAAGAATACATGGAAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGTCTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
TTTTATAGAAATCAATGATGGGTGAGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC
TTGTGAGTTTTATATTTTAAAGAAAGATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAAATGATTCAAAAAAATTAAACTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC
AACATTGTTTATATTTTTCTATTCAATAAAAAAGCCCTAAACAACTAAAATGATTGATTGTATACCCCACTGAATT
CAAGCTGATTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTTAATTTACAGCT
AAAAATTTTTTAAATGCATGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATTTTTTCAGAAGTTAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFFERSTIRSRSFKKINR
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVPSESLSIRLV
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNMGDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDIFQEAGWNSNGSWSPG
PGRSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR
IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAP
SDWSPSWMMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
CTTGCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
TTCCACCTTTCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTTCC
ATAAGACCCTCATTTTGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
GACAACGTGCTCTTCTGTGCTCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
TTTGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
CTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
CATCTGCATCCCTTCTGTCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
ACTGCTTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTGG
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACACTAGGGGAT
GGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCATGCACCC
TGGATCTTTTGGTGATGTTTGGGAAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA
ATAGTAGCACACATTAAGAACCTGTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTCT
TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATATTATGGGAT
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
AGGTACGAAGATACAATACTGTTATTCAATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGCAGGT
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
CTTCAGGGGAGGACCTGCCAGGTATGCCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
TTTTAAAGAGTTTTTGTAAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLTFFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWGGE
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

[illegible]

FIGURE 44

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCHRSKCGMCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG
GTCCTCCTGTGTCTCCTGTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCMEHGEEVDIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTATAGTCTATTGCTTGTGGAATTCTGGAGGTCCTGTTGGGCT
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCCEGWTSCNGFSLVLLVLLLVVNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNANCEFSL
KNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCCTTGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT
TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS
SQKQHSPVPEKAIPLITPGSATTG

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGACATGGCCTGGGAGACGCCCTGA
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCGAGCTGGCTCTAAAGTCAGTGAG
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA
TTGGCAGACAGGCAGAAGATGTCTTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG
GTGCTTGGCCACAGTGGTGCTTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG
CCTTGAGGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
TGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA
CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGAATCTGGGATTCAGGG
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
GCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACTCCCTCCTTAA
AACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTGAAATAAACCTTAGCTGCCCCACAAA
AA
AA

FIGURE 52

MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS
EALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVF
GHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPVWHGYPGNSAGSFGMNPQGAPWQGNGGPPNF
GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGGS
SSGSSSSGSSSGGSSGGSSGSGNSGSGSRGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNE
ARGSGESGIQGFRGQGVSSNMREISKEGNRLGSGSDNYRGQSSWGSGGGDAVGGVNTVNSETSPPGM
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCCGCCGGCTCCAGTGTTC
CACAGCCCCAAAACGGAAGTGGTTTTTGGGGTACCTGGGCCTGATCACTCCTACAGAGGAGGC
TTGAAGGACTCGACCCAGATGTGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGCTCTGGACATGTTTGGACACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCAT
CTTGAGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCCGCTGGTGCATGACTTCACAGAC
GCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTGAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC
TCCCAGTGTGCAACCCAGGACATTGTTCTCCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTCCGCA
GGGCCCAGGAAGTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCTTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCATGACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAACGGTGTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVGWSLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLG
LIPTTEGLKDESTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGEILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDLFDVLLLSKDEDEGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGCCGTGTGTCTTGC
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCTT
GTGATTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA
GCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGGAATCTTCCTCATGTACCTGTTTCCTC
TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA
AA

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGAGTGGAGCACCCAGCAGGCCGCCAACATGCTCTGTCTGTGCCTG
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC
ATTTTCAAGCTCAGTGTCTTATCCCCCTCCAGGAATTCTCCACCTACCGCCAGTGGGAAGCAGAAAAATGTACAAGCT
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAAATTTGCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG
CTGGTGTTTAAGATTTTGGACAAAAAGAAATGATGGACGCAATTGACGCGCAGGAGATCATGCAGTCCCTGCGGGACTTG
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCTCAAGAGCATGGATAAAAAACGGCACGATGACCATCGACTGG
AACGAGTGGAGAGACTACCACCTCCTCCACCCCTGGGAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCCACG
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA
CACCTGGTGGCAGGAGTGGGGCAGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG
CAGGTCCATGCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGG
TCACTCTGGCGGGGCAATGGCATCAACGTCTCAAAATGCCCCGAATCAGCCATCAAATCATGGCTATGAGCAG
ATCAAGCGCTTGTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCAGGGGCC
ATCGCCAGAGCAGCATCTACCCAATGGAGTCTTGAAGACCCGGATGGCGCTGCGGAAGACAGGCCAGTACTCAGGA
ATGCTGGACTCGCCAGGAGGATCTGGCCAGAGAGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTG
GGCATCATCCCTATGCGGGCATCGACCTTGCAGTCTACGAGACGCTCAAGAAATGCCTGGCTGCAGCCTATGCAGTG
AACAGCGCGGACCCCGCGTGTGTGTCTCTGGCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC
CCCCGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCTC
TTCAAACATATCTCGGACCCGAGGGGGCCTTCGGGCTGTACAGGGGGCTGGCCCCCAACTTCATGAAGGTATCCCA
GCTGTGAGCATCAGTACGTGGTCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTCCGGGTGACGGGGGAGGGG
CGCCCGGCGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACACT
AAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCCACCCGAGGGAGGCTGGGGAGAGCTGGCAGGCCAGGGCTT
GTCTGTGACCCAGCAGACCTCCTGTTGGTTCCAGCGAAGACACAGGCATTCTTAGGGTCCAGGGTCAGCAGG
CTCCGGGCTCACATGTGTAAGGACAGGACATTTTCTGCAAGTGCCTGCCAATAGTGAAGCTTGAGGCTGGAGGCCGGCT
TAGTCTTCCATTTCACCCCTTGACGCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGCATCTCCTGTGC
CCTCTTGTCTGCCTGCTGTCTGCTGAGGTAAAGTGGGAGGAGGGCTACAGCCACATCCCACCCCTCGTCCAATCCC
ATAATCCATGATGAAAGTGAGGTACGTTGGCTCCAGGCTGACTTCCCAACCTACAGCATTGACGCCAAGTGGC
TGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGCTCTCGGGCATG
CTTGGGAGTGAGGGGGCTCGGGCTGCCTGGCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT
GGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAACTCACTGTCCCCACTGTGGCATGAGGGCAGTGGAGCA
CCATGTTTGAGGGCGAAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAGGTGTGGAGGCCCTTAATTATGG
ACTGTTGGGAAAAGGTTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTTCCTGTCCAACCCAGCAGGGGGCGCAGC
GGGACCCAGCCCATCTCCACTTGTGTCACTGCTTGAACCTATTATTTGTATTATTTGAACAGAGTTATGTCTT
AACTATTTTATAGATTTGTTTAAATTAATAGCTTGTCAATTTTCAAGTTCAATTTTATTCATATTATGTTTATGTT
GATTGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCCGTGCAGTCACTCT
GTCCAGAGAAATTCCTTTTGGACTGGAGGCAGAAAAGCGGCCAGAGGCAGCAGCCCTGGCTCCTTTCCTTTGGCAG
GTTGGGGAAGGGCTTGCCCCAGCCTTAGGATTTCAAGGTTTGAAGTGGGGGCTGGAGAGAGGGAGGAACCTCAAT
AACCTTGAAGGTGAATCCAGTTATTTCTGCGCTGCCAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG
TGAGGTGCCTCTCACTGTGAATTTGTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGTCCTCCAGC
CTTCTGTGCTGCCCTTGCTTAACAATGCCGGCCAACTGGCGACCTCACGGTTGCACTTCCATTCCACCAGATGACCTGA
TGAGGAATCTTCAATAGGATGCAAGATCAATGCAAAAATTTGTATATATGAACATATAACTGGAGTCGTCAAAAAG
CAAATTAAGAAAGAAATGGACGTAGAAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAA
AA

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMWRRHLVAGGG
AGAVSRTCTAPLDRLKVLMMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGINVLKIAPESAIAK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTTCTGATAT
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
AGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTTGTGATCAAGTGATAGTT
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
CAGCCACAGTGCTTGGGCATCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATAC
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGTTGTGTCTGTGCTCTACAATGTTACGA
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
CTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
GTGCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTCAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACAGACAAAGTGTGTTAAGA
GTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
TGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCAC
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6o

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYMLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
GGGCTACCCCCTGGTGGTGGTTATGGGGGTCTGCCCCTGGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG
GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCCAGCAGCCT
GGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGGAAGAACCTCTT
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCAGTTACCCAGCTTCTGGTCTCCCGCTACTGCCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTCTTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAAATGG
AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCAAAGTGAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCATAAAT
CCTTGTTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTTGCATTTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC
AACTTGCCTCAGCTCGGACAACTTCTCCACTGGCCCCTCTAACTCTGAACATCCGCAGCCCGC
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTCTAATTCACTGGGAGCCGGGGGAAAAATCCTTTCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCTGGGGTACCCTGAATCCCAGTG
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAAACGAGGCCCATGCCACACCCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCTGGAGTTCTCCGC
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGCTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCTGCTCCCGCCCTTGCTG
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGILLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSQVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRP
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRMPHPGEGIWGINNQPPGTSWGNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCCTCCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCGACCCCTGTCTTTCAGCAGGCCCCCACCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MGSGPLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACCTTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLRLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLRKQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTTGTTTTCTCTAGTTCTGTGCCTGCTGCACCAG
TCAAATACTTCCTTCATTAAAGCTGAATAAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
TTTTTTTTTCAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAACATGAA
AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTCACA
GAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAAACAATAATGAATATGGACCA
CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT
CAAGGAGGCAGCTGCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAATGTATGGAAAAGATTGTCAATTCTTT
CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAA
AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAAT
TCTGAGGATTTAAAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAAGGACCGCTAAATCGAATGAATCAAGCAGCA
AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACCTTGTAGTACTGCCACTATTGTA
AATAAGCTAATCCAAATAAAAGCAGTGATGAAAGAAACACATCATGGCAGGATTACCTACATATCCTCTGGGAGGA
ACTTCCATCTGCTCTGGAATTAATATGCATTTCAGGTGATTGGAGAGCTACATTCCCAACTCGATGGATCCGAAATGTA
CTGCTGCTGACTGATGGGGAGGATAAAGTCTGCAAGTCTTGTATTGATGAAGTGAACAAAGTGGGGCCATTGTTTAT
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCAATTTTATGTT
TCAGATGAAGCTCAGAACATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATAGTATCTCTCCCAAGAG
TCCCTTCAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCTGGATGAACGACACTGTCAATTTGATAGTACA
GTGGGAAGGACACGTTCTTCTCATCAGATGGAACAGTCTGCCTCCAGTATTCTCTCTGGGATCCAGTGGGAACA
ATAATGGAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAAGTGCAGAGGTGGGCACT
TGGGCATACAATCTTCAAGCCAAAGCGAACCAGAAACATTAACATATTACAGTAACCTTCTCGAGCAGCAAAATCTTCT
GTGCCTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAACAGTTTCCCAAGCCCAATGATTGTTTACGCAGAA
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAAATGGACATACAGAAGTT
TTGGAACCTTTGGATAATGGTGACGGCGCTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT
ACAGAAAATGGCAGATATAGCTTAAAGTTTGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCTCCA
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAATTAAGCAAAACCCGCCAAGACCTGAAATGAT
GAGGATACTCAGACCCTTGGAGGATTTAGCCGCAACAGCATCCGGAGGTGCATTGTTGTTATCACAGTCCCAAGC
CTTCCCTTGCTGACCAATACCACCAAGTCAAATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATTCTT
ACATGGACAGCACCAGGAGATAATTTGATGTTGAAAAGTTCAACGTATATCATAAGAAATAGTGAAGTATTCTT
GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGAGGCCAACTCCAAGGAA
AGCTTTGCATTTAAACAGAAAATATCTCAGAAGAAAATGCAACCCACATATTTATTGCCATTAAAGTATAGATAAAA
AGCAATTTGACATCAAAAGTATCCAACTTGACAAAGTAACTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGAT
CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATTTCTACGCTGGTATTG
TCTGTGATTGGGTCTGTTGTAATTTGTTAACTTTATTTAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTTC
AAGTAGACCTAGAAGAGAGTTTTTAAAAAACAACAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT
GTGTGATCATAAACTCATAAAAAATTTAAGATGTCGGAAGGAGTACTTTGATTAAATAAAACACTCATGGATA
TGTAAGAACTGTCAAGATTAAATTTAATAGTTTCATTATTTGTTATTTTATTGTAAGAAATAGTGAACAAAG
ATCCTTTTTTCACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTTGCATCAA
GAAATTTAAATCATCTATCTGAGTAGTCAAATACAAGTAAAGGAGAGCAAAATAACAACATTTGGAAAAAATAAAAA
AA

[illegible]

Signal peptide:

Putative transmembrane domains:

Leucine zipper pattern.

N-glycosylation site.

Page 224 of 322

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN
TLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLF
SQYNPGIYGHHDVPPLEQQVLVKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYR
KYLHNSNLIVRTPVRGLFHLWHEKRCMDLTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEAHL
RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEAT
FAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHLHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEPSKLLV
QNYRALQPLNORMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGCTCCTGACAGCTCC
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACCCAGCAAATTT
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTGAGAACCAGTACATTTGTGCGGGGCTGAAGAGCAGGA
GCTCAGTTTGAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATACCCCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA
TCCCCAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA
TGTCGAGATGGAACATGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT
CTGTGAGAATTACTTATTTCTTTTCTTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHHPANLILYGNEDKRFFVPAEK
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPPDKTVIEYDYVRTTDICAGPEEQELSLQEEVSTQGTLLESQA
ALAVLGPQTLQYSYTPQLQDLDPQAQHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEAPDRPPGENETILMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
CTGGGAAGATCGGCCGCGCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
CAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
GGGAAAAGCCAGCCGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC
ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCAATGACCA
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
CCCCCGCCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACCTGCTGTA
TAAGCTCTCCTTCCCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGC
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
TCCTGCCATCAAGGGTGACACCATTACGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCCCTGTTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG
CCTTGGGATTCGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGCTTACTCCAGCCTCC
TTGTGGAAACCCAGCTCTCCTGTCTCCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACTTG
CCTGTGAAAAA

FIGURE 78

MAGPWTFLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAMREK
PAGGIPVLGSLVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYLGAKLLDSQGKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAALVSPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSILLPNQNGKLRSQVPSLVKALG
FEAAESSLTKDALVLTPASLWKPSSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGAGAGCCTCCTGGGATTC
ATTCTGTTCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTACCACTGGTGCCTGACAG
CATGAAATTTGAGATTGAGAGGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGAGAAATCGCTCCAATACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMTSSAIISSSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTT
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCTCT
GCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
GTTGATCTGTGGCCCCGTGCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
ACCAGCGGCCTGACCTGGGGAAGGATGTTCCCAGGTGAGGGTCTCTCTCTCTCTGCTGGGA
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
ACTGCCTGCCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGC
ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCC
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
AGAGGCCCCGGGCACCCCAAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT
GTGTGCATGGCGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
CACCGAGTACCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCCAGAGG
ACAAAGCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTC
CTCGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
GTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCACGAAGGTCCT
GGAACGTCTTCCTAGCCCAGACCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFFLD SHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHEL F
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYS
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAG
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTCACTCCTCGGGCTGGTTCCCCCGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTTGTCC
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGGACTGAAGATTTCTTCTCCAAATTCCAGTGGAATCCAGGCGGAAGTGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA
CTGGGAGGTGGACGGAGGACACATAAAAGGTGGCGCTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT
ACATTAAATCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCTTGACTA
TGAGTGTGGGACCATCTCCTTCTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCGGTTTG
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAATCCCATAGTCATCTGC
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG
TGAGTCCTCCTCACAGGAACACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG
AACCGTCAGGAATTCCTCTCACAGGCTGTGGTGTAGATTAAAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGDLSTDSRTNRDMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAPEVPHSEKRF
TRKSVVASQSFFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTSSESSSQATTPLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCTGCCCCCT
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT
TACCCTGGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
GGGACCCACATACCAAGAATTGCACCCGTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCC
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCGCTCCTCGGTGCTCACCCCTCATCCACA
GCCCCAGGACCATGGCACCAGCCTCACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCT
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA
GAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCT
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAG
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTT
AGCCTCTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAG
CTTCTGCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGAGAAGTCA
GAGGCTGATTCTTGTAGAATTAAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC
TCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPACEQGTTPMISWIGTSVSPLDPSTTRS
SVLTLLIPQPQDHGTSLTQVTFPGASVTNKTVHLNVSYPPQNLMTVTFQGDGTSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE
DANAVRGSSASQGPLETPWAEDSPDPQPPASARSSVGEGLQYASLSFQMKPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCAGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVIIPVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGC GGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTACAGCTGGTGGCCGCGCTCT
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCTTCTTCAT
ATTTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCCAGCTG
TCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTCATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPFTFTPEEYDKQIDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCGAACCACAGCCCCC
CACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTCGCTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTAC
CATAGTGATACCCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC
AGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCAGAGGGCTTGGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACGGGGTTCTCCCGGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTTGGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAAATCCCTTTTTCTGGTGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAFGPALALYVFTTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLGPGTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCCKKKWGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKNFLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCACAAAACCTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACA
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTAC
CAATTTTGTGCACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCCACCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
GAACCCAGCAGGCCGCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
TACCTGAAAATATTCTTGAAATTCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAACATATTTGGAAAACCTGGAAA
AAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTGACCATG
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGGCCAGCCTGC
 AGAGCTGTCTGTGGAAGTTCAGAAAATATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAGGGCCCTGGACCGAGAGGA
 GCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC
 AGAGCTCGGCTGAGCCGGGTACCAGGCCTGGCATCCCCCTTCCTCTTCTTGAGGCTTCAGACCG
 GGATGAGCCAGGCACAGCCAACCTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
 ACCAGCCTTGACCAAGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
 CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGAAGTCTCCATCATAGAGAGCACCTGGGTGT
 CCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGCACCACATGGCCCAGGTA
 CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGGACCCCTTGAAGTGAA
 TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCC
 AGGTGCGGGCTCAGAATTCCTATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTG
 ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCGGCTCCCCCA
 ATTTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACCTCCGAGCAGGCCAGAACAT
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
 TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCTGAGTTTCACTTCCAGATTGGGCCT
 ATAAGCCTCCCTGAGGATGTGGAGCCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
 CCTCGAGCCCCGCTTCCGCCCTCATGGATTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCCAAGTTGG
 ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTTCTGCTGACCATC
 CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
 CTGCATTGAGAAATTCTCCGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCCCTGTGCCCTCCCAA
 TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT
 GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCCAGTGAT
 CGTGTGTCGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA
 CGAAGCTGTGCGGAGTGGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCTCATCCTC
 ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT
 GAAGGCGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
 TCCCTTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCA
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAACTT
 TATGGACTGCCCATGGGAGTGTCCAAATGTCAGGGTGTTCGCCAATAATAAGCCCCCAGAGAA
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSVPQALPKAQPAELSVVPEVNYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI
YRRLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFMQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSIESTWVSLEPIHLAENLKVLYPHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADLEPAFRIMDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY
EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISTRFSLVNDSEGLWCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGYPSTLGPNTVQRDWRLQTLNGSHAYLTALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRNVEGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGCCTG
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCCTCTAAAGTCTTGGTAC
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC
TCTGCCAACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
GCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTACCAACT
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTACCAATTCTGAGTCCAGCACACCCTCC
AGTGGGGCCAAACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACAGCCAC
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
CACAGTGTCCAGTGGGATCAGCACAGTACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAACAGCAGCTCTGACTGGA
ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGTGAGGCAAGCCTGGTGGGTCCCTGGT
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCACAGGCCCAG
GTGGAGTCCCTAACTGGTTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
ACAGCGGGCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
CCCAAGACCTGGTTTCTTTTTCATTTCATCCAGGAGACCCCTCCAGCTTTGTTTGGATCCTGAA
AATCTTGAAGAAGGTATTCTCACCTTTCTGCCTTTACCAGACACTGGAAGAGAATACTATAT
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG
CCCCGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCATGCTGGACTC
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTMHHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVA
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVSII
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG
GGAGGCTGGAATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTCATGGAAAGGATTTACTTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATTT
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTTGGCAACATGGCTCACCCCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGT
GATTATAACTGGGATGCATTTGTTCTGGAGAAAGAGTGTCATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGTTGGTGGGCCATGCAGGCTGCTGCCTATAT
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTCGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCATTCCACCTTGCAAGTCTGAAGTCTCAGGGTC
CTTGTGGTCAAATGCTCTCTATACTGTATTGGACCCTGTTGAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTGCATGACTATGTCGAATATTTCTTACT
GCCATCATTATTTGTTAAAGATATTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

FIGURE 102

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSI FMLSP
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
FLWNCMLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP
LQLLIFPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLQGDFFPREIH FHVHRYPIDTLPTSKE DLQWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPPCKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG
LEIIE LACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTTGCTGTCTCAGGCTGGTTCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
AGGATTTTGTCTTCAGACTCCAGAGCAAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCATCCACCTTGCTGAGCAGAGTCATGA
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCTGGCTTCTA
TTTTACTCGGGTTACTCTGTGGTGGCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCGCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAAGTGAACCCATAGAAAAGCTCCCGAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACA
ATGTGACTTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTC
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
TGACATGTCAGTTTGAAGGCTTGGTTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT
TGAGGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTTCCACCATAAACTCTGTT
TGCTTATTCCACATTAATTTACTTTTCTCTATACCAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAAACCAGGCAAGAAAACAGAAGAAGAGGAAGGAAACTACAGGTCCATATCC
CTCATTAACACAGACACAAAATTTCTAAATAAAATTTTAAACAAATTAACATAAATAATTTA
AAGATGATATATAACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAAATTTAAAT
ATCAACCAGTGTAATTACGACATTAATAAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLSFYELVSGWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPOEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
TTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGCTCCTGGCAGTGTGCATTGGA
CTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCAATTTACAAC
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
AGTCAACAGAAGCATGGAGTGTGGGTCATATGCTGTTGATTGTAGATTCTACTCTACTGAGGATCCTGA
AACTGTAGATAAAATGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAAGTAGAAGAGGGTGAATG
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
TTGTGAGTGTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
ATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA
TGACTATGATATTTCTCTTCAGAGCTTTCTAGCCCTGTTCCTTACACAAATGCAGTACATAGAGTTTGTCT
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTGGAGCACTGAAAAAT
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
GCCAGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
AGCTGGGGAGATGAATGTGCGAAACCCCAACAGCCTGGTGTGTTTACTAGAGTTACGGCCTTGCCGGGACTG
GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTGTTTTTTG
GGTGTGGAGGCCATTTTATAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
GATCAACTCTGTCTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
ATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTGTGAGAATTTGACTTGTGACATAAATTTGTAAT
GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCCTCAGCTCCTCTCATTTCAGCAAATATCCATTT
TCAAGGTGCAGAACAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACA
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG
ATATATCCTTATTTTCATTTCCAAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSPVYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCTG
CCCCGATGAGCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCCCAGC
GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
ACGGGGCTCACAATGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA
TCTGCTCTTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGACTACCTAA
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCTT
GTGGTTCATCCGGTCATGATTGCTGTTTCTGTTTCTTATCATTGTGGGGATGTTAGGATATTG
TGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGTCTGTCATTTTCT
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCAGTACAATGGTCA
GATATGGTCACCTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA
TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGTGAGTAGTATATTTCACTGACTGGTTGG
AAATGACAGAGATGGACTGGCCCCAGATTCCCTGCTGTGTTAGAGAATTCCAGGATGTTCCAAA
CAGGCCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCTT
TTTGAGAGGAACCAACAACATGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
TCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGAGCCTGGG
ACAGACCAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCTGTCCTCAGTAGAACT
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
TTGAGATGGAGGAGTTATATAAAGAAATGTCACAGAAGAAAACCAAACTTGTGTTTATTGGACT
TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA
TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC
ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGTTGATTTACTTCTACCAA
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTTCAATATTGGTGACT
ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACCTAAAAGAGCAAGCTAACACAT
TGCTTAAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT
ATTTTGTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAAC
TGTTATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA
AAGGACTTGTATGCTGTTTTTCTCCCAATGAAGACTCTTTTGTGACACTAAACACTTTTTAAAAA
GCTTATCTTTGCCCTTCTCCAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTCTACAGAAAA
TAGTGTCTTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT
CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAA
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTAT
TTCTCAGAATATGGAAAGAAAATTAATGTGTCAATAAATATTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTCCTCTGATAAAGCCCCCTACCAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTTCCAGTGTCTTCTGGCAGTTGGTCCAGAAGGATGCCCTCCATTCTCTGCTTCTCACCTG
CCTCTTCATCACAGGCACCTCCGTGTCAACCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACCACTTGGATGAGTCTCAAGGTCTCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACCTTACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAAGTGTCTCTCTGGAACACCACGGTGGAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTATGACATCTGCGACGAGGACTGCCATGG
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTTACCGCTGT
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGTGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCCTGGTGTGT
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGGTTGGTGGCCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCAGCCATGTCAACAT
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCCAAGCAGACCCCCGGGGAGCAGCGGGGACTTCATCATCCGAACAGCAAGCTGCTGATCCCGGTG
ACCTGCGAGTTTCCACGCTGTACACCACTTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT
CATGAGCCGAAATCATGGGATCTTCCCATTCCTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTGCACGTGCCGGTTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGCGAATGCGTCTGTGGGCAGGAGGAGGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGCGGGCCGATCCGCATCGACTGGGAGGACTAGTTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCGCCCTCTAAGAACATCTGCCAACAGC
TGGGTTTCAGACTTCACACTGTGAGTTTCAGACTCCACGACCAACTCACTCTGATTCTGGTCCATTCAAGTGGGCA
CAGGTCACAGCACTGCTGAACAATGTGGCTGGGTGGGTTTCATCTTTCTAGGGTTGAAAACCTAACTGTCCA
CCCAGAAAGACACTCACCCATTTCCTCATTCTTTCTTACACTTAAATACCTCGTGTATGGTGAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTCAAGTTACAAACCCTAGAAAAATTAACAGTTACTGAAATTATGA
CTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA
TTATAGGGAATTTGGAAGTGTATCAATAAACAGTATATAATTTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLQDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSNHTCQVPVLCKSNAIEVNI PRELVGG
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVDVVDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEPEPYREALPTLKLKRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGGCHRRMRGAGGEDSAGLQGQTLTGGPIRIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
GGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
AGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTG
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCTGGACCCCCACTGGGTCTCAAGGCA
GCCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAG
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATGAATTCAACCCCATGTACCCCAAGACATGACA
TCGCCCTCATGAAGCTGCAGTTCCTCACTACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
GATGTCTGACATACTGTGTCAGGCGTCAGTCCAGGTCAATGACAGCACACGGTGAATGCAGACGATGCGT
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGT
GACAGTGGTGGGCCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
CTGCGGGGGCCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
TTCTTGAGCAGCAAAGGGCCTCAATTCCCTGTAAGAGACCCTCGCAGCCCAGAGGCGCCCAGAGGAAGTCA
GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCC
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
ACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAA
AAAA

FIGURE 112

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPITIIALLSLASIIIVVLIKVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAEACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGGEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAHCFRKHTDVFNWKVRAGSDKL
GSFPSLAVAKIIIEFNPMYPKDNNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQDSSGGPLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAAGTGTCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAAATC
TGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACCTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCCGAAGATTTTCATAGGCGATGGCTCCCCTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCGTGGACACCTGTCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTTCATGTCCTGCACATCACCTG
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTGAGAAAAGATG
GAGGTGTTGGGTATCACAAAGGCATCGAGTCTCCTGCATTCAGTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTTGGCCAGGAGGTGAGCAAGGCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAGGAGCTAGAGCTTGGTT
CAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA
TGTTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAAGTAAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGAGAGAAGATCTTCACTTTCCTGCCAACGAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTGCTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAYDME
HTFYSGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGGCGGGCGGCCAGGATCATGTCACACCACCATGCCAAGTGGTGGCGTTCCTCCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGTGGAGTG
TCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTTCGTGGGCTGGGTGCGTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCAACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCAGCACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGTCTTTGACTCACAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTGAAGGAAA
GAGTAGACCCAAAGATGTTATTTTCTGTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTAAGTCCATAATATAGTTAA
AATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCA
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC
AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTATGCCTCAGTGGAGAGTGTGGCCTTCATT
GAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG
GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA
ACTCAATAGTGAATGTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
CTGGTGTGCTGATTGTTGGAGGAGCTCTGTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTA
CAGATACTCGATACCTTCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAGTCAACGAGCG
TCTACTCCAGAAGTCAGTATGTAGTTGTGTATTTTTTTAACTTTACTATAAAGCCATGCAAATG
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT
AATCTTAATTACAGGAACGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGAGAATGAGATA
TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
CTCTTTTTATCATTACTTCAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTTCTCC
ACGACATAGCATTATGTACATAGATGAGTGAACATTTATATCTCACATAGAGACATGCTTATATGGT
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCACTATTGCTTTTCAGGGAA
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGCTCCTCCA
TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATGAATGGCTTTCTGATAT
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT
CTTGTGTATTAAATTAACATTTTAAAACGCAGATATTTTGTCAAGGGGCTTTCATTCAAACCTGCTT
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
AAAAATTTTTGTTTTTGTATTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA
TGCTTGGTTTTTCATTGCTTACCAAAAAACAACAACAAAAAAGTTGCTTTGAGAACCTCACCT
GCTCCTATGTGGGTACCTGAGTCAAAATGTCATTTTGTCTGTGAAAAATAAATTCCTTCTTGTA
CCATTTCTGTTTAGTTTTACTAAATCTGTAAATACTGTATTTTCTGTTTATTCCAAATTTGATGAA
ACTGACAATCCAATTTGAAAGTTTGTGTGACGCTCTGTCTAGCTTAAATGAATGTGTCTATTGCTT
TATACATTTATATTAATAAATTGTACATTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK
IYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGMKTRCTGDNEKVKAHILLTAGIIFIITG
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG
CCAGACGCTGACCACGTTCTCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCGGCGAGCC
GGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCTCTGCTGCTCC
TGCTGCTGCAGCTGCCCCGCGCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTGCGGATG
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCTGGACACCCAACTAC
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAATGCA
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCC
TTGGAATGGTTCACCTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTCTTTCTCTTAGTATAGCATTTTAA
AAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGVPGR
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMNSTINIHRTS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
CTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
ACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
TATTACCTAGGAAGATTTTGTATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
TGTTCTGCGTGGCTGGCAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
TCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTATGCAACTG
GCCCCAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTTCAATG
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCCACTGTCTTACTGACAATG
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCCAAAATGGTATATTGTGA
ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGA
GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATT
TACGGAAGCTTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
CGGAAGCTGTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGGAATATTTCCA
AGACTGCCGCAACCTGGAAGCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAAC
CTGGCCCTTTTCCAAGGTTGGTCAAGCTTTCAGACCTTACAGAACCTTTACTTGCAAGTGAATAAAATCAGTGT
CATAGGACAGACCATGTCTTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
TCGAAGCTTTTCAAGTGGACCCAGTGTTCCTCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT
TCCAACAAGCTCACATTTATTTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTGAAAAGTT
TTAAAGGTCTAAGGGAGAATAACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGTATCTGGCCAG
GGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCCCTT
TGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCCCTGTCCGTGCTCGTCATCCTGCTGGTTAT
CTACGTGTCTATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
GGCAGAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTA
GATTATAAACCCACCAACACGAGAGACCGAGATGCTGCTGAATGGGACGGGACCTGCACCTA
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAGCT
GGGAAATAAGTGGTGTCTTTATTGAAGTCTGGTGAATCAAGGGAACGCGATGCCCCCTCCCC
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCCGTTTTAGTGCATTATAATACT
GGTCATTTTCCCTCTACATATAATCAACCATTTGAAATTTAAATACCACAATCAATGTGAAGCTT
GAACTCCGTTTAAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAATGTGCGATTT
GTTTTAAGATAAACTTCTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLSSLHLRSNSLRTIPVRIFQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSTWSSSLQRLDL
SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG
ATGAGCATTATCCCCTTTGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
TTAGCCAATCCAAGTACCTAGTGAAGGTTGAGATGCAAAATGGAAGGAAAAAGGAACTGGAAGG
AAAACCATTTGCGATTTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTCAAGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

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FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGCGGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC
CCCCGTGTGCGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACTTTGATCCCCTACAGATGTGACCTAT
CAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCGGCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTGA
CCCCGTGTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCCCTCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT
CACGGGATACCACTTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGTCCTTGGCCACTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCCAGTCTTGGCTTCTTGTCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCAGTGGATTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAA
AAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAAVARALVQQLKVVGCARTVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLTLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININMSGHRVPLSVTHFYATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGTGCAGAGTCTCAGTTGCCCGGGAGC
ACCTCCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTTCAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAATTGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTCTCATTTATTTA
TTAATTTTTTAAGTATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAAGTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAAGTCTCGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAGTGTATGATTACA
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGGAACTTTGAAATTAT
ACAATGAATTATTGTTAACTGTCTCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAAATGACAGGATTCGTTCTTAATTTCAATTAAATAACCACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGGHTLGESMPFVKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAATAAATAATGCTGGGATTCCTTCAGAT
TTGAAAACTTGCTGAAAGTAGAAAGATATACCTATACCACAACAGTTTAGATGAATTCCTACCAACCT
CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATCCCTGGGGTTT
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTCAAG
GTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCTGGTGGGGAATTCCCTGACTGCTGCACCAGTAAACCT
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
AGGTTCTGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAACCCACAGGGAGTCCCTCAAGAAAAA
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTATCTCTTGGAACCTTGCTCTACCTATG
ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCCATATAAAGTATGCATGGTTC
CCATGGAACCCAGCAACCTCTACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTT
CGAATGTACAACCCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCCAATTTACC
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGTATG
TTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
GCAGAAGCTGGCACTAAGAAGGACAACCTATCCTGGAATCAGGGAACTTCTTTTCAGATGTTACCAAT
AAGCAATGAACCCATCTCGAAGGAGGAGTTGTAATACACCATATTTCTCCTAATGGAATGAATCTGT
ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL
EELHLD DNSVS AVSIEEGA FRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAA PVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGWPA PVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKS VTSDTIHISWKLALPMTALRLSWLKLGHSPA FGSITET
IVTGERSEYLVTALEPDS PYKVC MVP METSNLYLFD ETPVCIETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIAL LALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLYKNNHSESSSNRSYRDSGIPDS DHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGCA
GCCCTGCCGGGCCACTTGTCTTCATGCTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGTGAGCGTGTGACCAGCAGTGAGCAGAG
GCCGGCCATGGCCAGCCTGGGGCTGTCTGCTCCTGTCTTACTGACAGCACTGCCACCGCTGTGGT
CCTCCTCACTGCCTGGGCTGGACACTGTCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
GCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCAGGAGCCCCCTGC
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCTCCAGCCCGG
GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGC
CCCAGGACTCATTTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
GACAGCAGCGAGCCCTGCGGCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
AGGCTACTGCCTGTCCCACCACTGCTCTTCTCCTCTGGGCCAGAATGAGGGGATGCACACAGG
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
AGAGCTGAGGCCATCGGATACGCCTACCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTCCAGATTCTCGCTCTGT
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC
AATTCTCTTGCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTCTTGCCACCCAGCACTC
ATGGGGGCTCTCTCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG
GTGGCTTCCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

FIGURE 134

MSARGRWEGGRRACRGSGLARAQGAERVTSSEQRPAMASLGLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRLVEEQKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSSPECGLSDLCSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCMGGFSDFYKLRWLEAILSQKQEGCGF
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTCAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEAGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLLKTDGSEFVVDIPSGSYVVEVVSAPAYRFDVPRVDITSKGMRRARYVNYIKTSE
VVRLPYPLOMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCAAAACAA
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCCTCTAGTCTTGCCCTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGIATTTAA
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
CTTCCTTGATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA
ATGTATTTATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAATTTTGTAAATCTAGAAGAGTGG
CTAGGGGGGTTATTCATTTGTATTCACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGTATGTGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCAATTTGTGTATCTTCCAG
CCAGGAATCTTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAA
AAAAA

FIGURE 138

MRQFPKTSFDISPMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

[illegible][illegible]

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLED SVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT
TCCCTATAGAAAACAACGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAACTACATACGCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAAC TAATTGTATAAAAAACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLD SGNLI AVDPKNYIRPEI
FFALASSLSSASAEKGSPI LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCTTCCTGTCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC
CTGGCATTTCACGAGCAAAGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG
AGCTGAACAATACTTTCACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTTGTCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTTTGTTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAA
AA

FIGURE 144

MLGLPWKGGLSWALLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACC GCCCGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCAACATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACCTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTTACAGATAAGGAAACTGAGGCCCGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATT
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTTCAGAAGCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTTCATTTTGCTTGTTCAGTGGGGTAGGTCACTGAGTCTTAGTTTTATTTTTTGAATTT
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTATGAGTATATTGCATTGATGTCTGAGG
TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCGCGCGCGCCCCAACCTTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC
CGGCCCCCTCTCCGCCCCACACCCACCTCCTGGCTCTTCTGTTTTTACTCCTCCTTTTCATTGATA
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGAAGAATGGGGTT
CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCCCATTCAAGCTTTCCCCAACCTGGAGGAA
GCCAAGACAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACTG
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCACAAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTGAGGAACCTCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAGAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCCAAGG
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLPIQAFKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLTLTNGLE
RRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEEAAMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHKDKGNKEDYDLSKMRDFINKQADAYVEKGILDK
EEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
GATGGTTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACCAAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCGTATCCTGGGTGTCCAGGGTGGAAAG
CCAGTGCCTGTCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCTGTGCACGGTGCCTGAAGCCGATCAGCC
TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG
TGGGCACCTGACCACCTTTGTCTTCTGGTTCCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT
CCACGGTCCTCCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTAAAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGCT
TAATGGTAAGTACAAGTGTACCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA
GGGTCAGTAGCTCTCCACATGAAGTCCTGCTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCATA
TGCTACCTTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTATGTAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
GATACAATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTATGACATATTGAGA
AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAATTAAGATACCTATTTATATATT
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTAT
AGGTGATTTTTCTTTAATTCTGTTAATTATCTGTATTTCCTAATTTTTCTACATGAAGATGA
ATTCCTTGTAATAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCCTCAGCCTCCACTTCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGATCAGGAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACAATAATCATCTGGTAATCTTTTCTAGAA
GATCACAGCCCCCTGGGATTCGAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCAATAT
GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGAAGAGGCAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCTGAACGAAGAAAGAATAAATTTCCGCTGTTTTAA
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAATGATCCCTGT
CTCCTCGTGTTTTACATTCTGTGTGTGTCCCTCCACAAATGTACCAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTGGTCTAAGTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILGVQGS
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGGWNAIPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCCTGGCCACCAGCTGCCTCCTTCTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACCTTACCCTTGAAGAAGTGTGTTCCCTCAATCTGATAGGTTC
CAGCCTTATATGCAGGAGGTGGTGCCCTTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACAAAAGGAAGATGGGAAGCCAAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
CAGTCAGTGCCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTCAGTGCAGAGGGC
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCCGT
TGCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGT
GTGATGGGCTTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTTGCCCCCTGTGAAGTGTGTCTGGAGCAG
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTGAAAAGAG
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTCAA
GTTCTGCCCATTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTG
GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT
TGTTTGTCTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPKSGQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTGKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGGAAGGCCACCAA
GATTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAA
AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA
GTAGAAGTGAACCTCACAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCAGAGTGAGGTGATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTCCCCCTTGCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLDLRLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFFVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD
GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACCTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 16o

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVSMsrNIESRSTSPWNYVTWDPNRYPSVVQAQCRNLGCINAQKEDISMNSVPIQQETLVV
RRKHQGCsvsFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

A C A C T G G C C A A A C A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A G G
 A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G A T T C
 C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G C A G C A C
 A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C T G T G C C C T G G T T C T G C T G T C C T
 T G G C A C T G G G C C G A A G C C C A G T G G T C C T T C T C T G G A G A G G C T T G T G G G G C C T C A G G A C G C T A C C
 C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T G C C T G G G G A C A T
 C G T G C C T G C T C C G G G C C C C G T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T G G T G C T G A G G T G C C
 A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G C C C G T G C A T G G G C A C T G G
 G A A G A G C C T G A A G A T G A G G A A A A G T T T G G A G G A G C A G T G A C T C A G G G T G G A G G A G C C T A G G A A
 T G C C T C T C T C C A G G C C C A A G T C G T G C T C T C C T T C C A G G C C T A C C C T A C T G C C C G C T G C G T C C T G C
 T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G T A T A T G A C
 T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A
 G G A A C T C A A C C A C A C A C A G C A G C T G C C T G C C C T G C C C T G G C T C A A C G T G T C A G C A G A T G G T G A C A
 A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G T A C T G G A A T C A G
 G T C C A G G G C C C C C A A A A C C C C G G T G G C A C A A A A A C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A
 C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A
 C G A A C A T C T G C C C C T T C A G G A G G A C C C C G C G C A C A C C A G A A C C T C T G G C A A G C C G C C C G A C T G
 C G A C T G C T G A C C C T G C A G A G C T G G C T G C T G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T
 G T G C T G G C G G G C T C C G G G T G G G G A C C C C T G C C A G C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G
 T C A C T G T G G A C A A G G T T C T C G A G T T C C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G
 A A C A G C T C G G A G A A G C T G C A G C T G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A A G A
 C G A T G T G C T A C T G T T G G A G A C A C G A G G C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A
 G T G G C T G T A C T T C A C T A C C C A G C A A A G C C T C C A C G A G G G C A G C T C G C C T T G G A G A G T A C T T A C T A
 C A A G A C C T G C A G T C A G G C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G
 C C C C A T G G A C A A A T A C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G
 C T G C G C T T T C C C T C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A
 C A G G A C G T C C G C T C G G G G C G G C C G C C A G G G G C C G C G C G C T C T G C T C C T C T A C T C A G C C G A T G A
 C T C G G G T T T C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G
 C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G C C C C G T G G C T T G G T T T C A C G C G C A G
 C G G C G C C A G A C C C T G C A G G A G G G C G G C G T G G T G G T C T T G C T C T T C T C C C G G T G C G G T G G C G C T
 G T G C A G C G A G T G G C T A C A G G A T G G G G T G T C C G G G C C C G G G G C G C A C G G C C C G C A C G A C G C C T T C C
 G C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G G
 G C C T G C T T C G A C A G G C T G C T C C A C C C G G A C G C C G T A C C C G C C C T T T T C C G C A C C G T G C C C G T C T T
 C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C G T T C C G
 G G C G G C T C C A A G A G A G A G C G G A G A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C
 C A T C C C C C G G G A C T C C C G C G C C G G G A C G C G G G T G G G A C C A G G G C G G G A C C T G G G G C G G G G A
 C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T C T A A A A A A

FIGURE 162

MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAGPVLAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTFQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVSDGDNVHLVLNV
EEQHFGLSLYWNQVQGPVKPRWHKNTLGPQIITLNLHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLTLQSWLLDAPCSLPAAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSICALEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT
LPSQLPDFLQALQPPRPRSGRLQERAEQVSRLQPALDSYFHPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTTGA
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTGACGGGATCACCCGGAAGTCCTGC
AACCTGACGGTGGAGACGGGCAACCTCAGGAGCTCTACTATGCCAGGGTCACCGT
GTCAGTGGGGAGGCGGGTCAGCCACCAAGATGACTGACAGGTTGAGTCTCTGCAGCACACTAC
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA
CCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTGGAAGACATCTTCCATGACCTG
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTTGCGTTCCCA
CCTGGGCCAAGGAGAGTGGCCCTTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
TACTCCTTCTCCGGAGCCTTCTGTTCTCCATGGGCTTCCTCGTCGAGTACTCTGCTACCTGAG
CTACAGATATGTACCAAGCGCCTGCACCTCCCACTCCCTGAACGTCCAGCGAGTCTGACTT
TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC
AGTCTGGCCCCAGCCTGTCCAGTACTCCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC
TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCAAACGCTGCCCCCTGAG
GTCGGGCCCCCATCCTATGCACCTCAGGTGACCCCGAAGCTCAATTCCCATTCTACGCCCCACA
GGCCATCTCTAAGGTCCAGCCTTCTCCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCCTAAA
CACCTTAGGCCATAAGGTACGCTTCAGAAAGAGCCACCAGCTGGAAGTGCATGTTAGGTGGCCT
TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
CCCTGGGGATTTCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG
GAGCAGCCACAGAAGTGGATTCTCTTTTCAGAGGCCTGGCCCTGACTGTGAGTGGGAGTCCCTG
AGGGGAATGGGAAAGGCTTGGTGCTTCCCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
ATCCCATGCCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGCTCGTGAGCCCTG
CAAGGCAGAAATGACAGTGCAGGAGGAATGCAGGGAAGTCCCGAGGTCCAGAGCCCCACCTC
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTTGCCAGTTTC
ACATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTCAATTGTCAAAGGTGGGAAGAGA
GCCTGGAAAAGAACAGGCCTGGAAAAGAACAGAGGAGGCTGGGCAGAACAGAACACCTGC
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCTGCAGTCA
TTCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTTCAGCTTCATTCTCTGATAGAACAAGC
GAAATGCAGGTCCACCAGGGAGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCCT
ATCCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC
TGTAAGTGTACAACTTTGCAAGCTCTGCCTTGGGTTGAGCCCATCTGGGCTCAAATTCAGC
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCGAGAACCTCGGTTTCCTC
ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
TCTTTAAAGTGCTTAATAGTGCTTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTPVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTelyarvtavsaggrsatkmtDRFSSLQHTTLKPPDVTcis
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRtyQmHLGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCrvKTLpDRTWTySFSGaFLfSMGFLVAVLCyLSYRYVTKPPAP
PNSLNVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPQILSPLSYAPNAapeVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM
EESQEAKSLHQPLGICTDRSDPNVLHSGEEGTPQYLKGQLPLLSSVQIEGHpMSLPLQPPSGPC
SPSDQGSPWGLLLESVCPKDEAKSPAPETSdleQPTeLDSLFRGLALTvQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAGTCACCCGGGCGCGGTGGCCACAACATGG
CTGCGGCGCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACCTTGGGCTGGA
AGTGTGTAACACAGTTTTGGATATTTTCCAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCCTGTGCCTGAGCCCGAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA
ATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGC GTTATT
CATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA
CTAAGCTGCCTTGGCAGTTGCATTTTTGAGCCAAACAAAATATATATTTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEECSMLMYRGKALEDFTGPD CRFVN
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPAETDFVCFEGGRD
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRA SEDGE GA
FSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER
EKTDAYKVLKTEMSQ RSGGQCVIHYSKGFRWHQNL SLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTAGAGGCCGGGGAAGAGAAGCAAAGCGC
 AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCTAAC TTC
 AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
 CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCCGGCAGCTGGGCTCGGGC
 GGCGGGAGTAGGGCCCCGCCAGGAGGCAGGGAGGCTGCATATTAGAGTCGCGGGCTGCGCCCTG
 GGCAGAGGCCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCTGG
 TCTCGCTGCTGCTGGGCGCCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCGCGTGGTCAGC
 GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCTACTTCCATGAAGT
 GTCCAGCCGAGTGAGCTTTTCCAGGAGGCACGCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCTCA
 GCCTTGAGAAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
 ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAACATCTGG
 TGCTTGCCAGATCTCTACAGTGGTCTGATGGAAGCAATCCAGTACCGAAACTGGTACACAG
 ATGAACCTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGC
 CTTGGGGGTCCCTACCTTTTACCAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG
 CAAGTATGAACCAGAGATTAATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG
 GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAAATCCCAATCTAATTTATGTTGTT
 ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGAACCTGTTGTTTCCAGATGCT
 GCATAAAAAGTAAAGGAAGAACAACAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA
 CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGAATTTCT
 GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAATCACAAGGATCTGC
 AAGATGAAGTGAAGCTCCCCCTTGAGGCAAAATATTAAGTAATTTTTATATGCTATTATTTCA
 TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTAAAGGATGCACCCAA
 ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
 TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAA
 TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTTTGATAAAA
 ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG
 AAACCTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
 TTTCTCGAAATAATTCATCTTTTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
 AATAAGAAGCTATTTTCAATTAAGTGTGATATAAACCCTCCTCAAACATTTTACTTAGAGGCAAGGAT
 TGTCTAATTTCAATTTGTGCAAGACATGTGCCCTTATAATTATTTTAGCTTAAATTAACAGATT
 TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
 TGACATACACAATATAAATCATATGTCTTACACGTTGCCCTATATAATGAGAAGCAGCTCTCTGA
 GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTCCGGGGTTTGGG
 ATTGACACTGGAGGCAGATAGTTGCAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
 ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
 ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTGG
 AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTT
 CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCCTTGTCTTCTCAAGAGAAAAGTTGTAACCTC
 CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTGGGGGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFCRVSVSGQKVCFAFKHPCYKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKTSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217